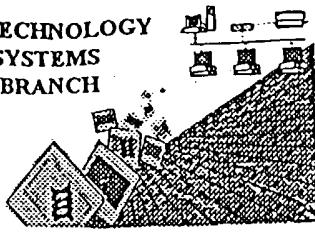


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/680,963
Source: IFWQ
Date Processed by STIC: 12/21/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/680,963</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text , as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue . Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input checked="" type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) <u>7-8</u> <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	<i>← This is the valid format for intentionally skipped sequences.</i>
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004

TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
 Output Set: N:\CRF4\12212004\J680963.raw

3 <110> APPLICANT: GlycoFi, Inc.
 4 Bobrowicz, Piotr
 5 Hamilton, Stephen R.
 6 Gerngross, Tilman U.
 7 Wildt, Stefan
 8 Choi, Byung-Kwon
 9 Nett, Juergen H.
 10 Davidson, Robert C.
 12 <120> TITLE OF INVENTION: N-Acetylglucosaminyltransferase III expression in lower
 13 eukaryotes
 15 <130> FILE REFERENCE: GFI-108 CIP
 17 <140> CURRENT APPLICATION NUMBER: US 10/680,963
 18 <141> CURRENT FILING DATE: 2003-10-07
 20 <150> PRIOR APPLICATION NUMBER: US 10/371,877
 21 <151> PRIOR FILING DATE: 2003-02-20
 23 <150> PRIOR APPLICATION NUMBER: US 09/892,591
 24 <151> PRIOR FILING DATE: 2001-06-27
 26 <150> PRIOR APPLICATION NUMBER: US 60/214,358
 27 <151> PRIOR FILING DATE: 2000-06-28
 29 <150> PRIOR APPLICATION NUMBER: US 60/215,638
 30 <151> PRIOR FILING DATE: 2000-06-30
 32 <150> PRIOR APPLICATION NUMBER: US 60/279,997
 33 <151> PRIOR FILING DATE: 2001-03-30
 35 <150> PRIOR APPLICATION NUMBER: PCT/US02/41510
 36 <151> PRIOR FILING DATE: 2002-12-24
 38 <150> PRIOR APPLICATION NUMBER: US 60/344,169
 39 <151> PRIOR FILING DATE: 2001-12-27
 41 <160> NUMBER OF SEQ ID NOS: 101
 43 <170> SOFTWARE: PatentIn version 3.2
 45 <210> SEQ ID NO: 1
 46 <211> LENGTH: 3
 47 <212> TYPE: PRT
 48 <213> ORGANISM: artificial
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Glycosylation target
 54 <220> FEATURE:
 55 <221> NAME/KEY: MISC_FEATURE
 56 <222> LOCATION: (2)..(2)
 57 <223> OTHER INFORMATION: wherein "Xaa" is any amino acid except proline
 59 <400> SEQUENCE: 1
 W--> 61 Asn Xaa Ser
 62 1
 65 <210> SEQ ID NO: 2

pp 1-3,6
 Does Not Comply
 Corrected Diskette Needed

give source of genetic material
 (see item 11 on Error Summary
 sheet)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004
TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

66 <211> LENGTH: 3
67 <212> TYPE: PRT
68 <213> ORGANISM: artificial
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Glycosylation target *same error*
74 <220> FEATURE:
75 <221> NAME/KEY: MISC_FEATURE
76 <222> LOCATION: (2)..(2)
77 <223> OTHER INFORMATION: wherein "Xaa" is any amino acid except proline
79 <400> SEQUENCE: 2

W--> 81 Asn Xaa Thr

82 1
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 21
87 <212> TYPE: DNA
88 <213> ORGANISM: artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,6-mannosyltransferase)

93 <400> SEQUENCE: 3
94 atggcgaagg cagatggcag t 21
97 <210> SEQ ID NO: 4
98 <211> LENGTH: 21
99 <212> TYPE: DNA
100 <213> ORGANISM: artificial
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,6-mannosyltransferase)

105 <400> SEQUENCE: 4
106 ttagtccttc caacttcctt c 21
109 <210> SEQ ID NO: 5
110 <211> LENGTH: 26
111 <212> TYPE: DNA
112 <213> ORGANISM: artificial
114 <220> FEATURE:

115 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,2-mannosyltransferases)
116
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (9)..(9)
122 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
124 <220> FEATURE:
125 <221> NAME/KEY: misc_feature
126 <222> LOCATION: (12)..(12)
127 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
129 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
131 <222> LOCATION: (18)..(18)
132 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
134 <400> SEQUENCE: 5

W--> 135 taytggmgng tngarcynga yathaa

26

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004
TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

138 <210> SEQ ID NO: 6
 139 <211> LENGTH: 20
 140 <212> TYPE: DNA
 141 <213> ORGANISM: artificial
 143 <220> FEATURE:
 144 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,2
 145 mannosyltransferases)
 148 <220> FEATURE:
 149 <221> NAME/KEY: misc_feature
 150 <222> LOCATION: (6)..(6)
 151 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 153 <220> FEATURE:
 154 <221> NAME/KEY: misc_feature
 155 <222> LOCATION: (12)..(12)
 156 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 158 <400> SEQUENCE: 6
 W--> 159 gcrtcncccc anckytcrt 20
 162 <210> SEQ ID NO: 7
 163 <211> LENGTH: 0
 164 <212> TYPE: DNA
 165 <213> ORGANISM: Kluyveromyces lactis
 167 <400> SEQUENCE: 7
 W--> 168 000
 170 <210> SEQ ID NO: 8
 171 <211> LENGTH: 0
 172 <212> TYPE: PRT
 173 <213> ORGANISM: Kluyveromyces lactis
 175 <400> SEQUENCE: 8
 W--> 176 000
 178 <210> SEQ ID NO: 9
 179 <211> LENGTH: 458
 180 <212> TYPE: PRT
 181 <213> ORGANISM: Saccharomyces cerevisiae
 184 <220> FEATURE:
 185 <221> NAME/KEY: MISC_FEATURE
 186 <222> LOCATION: (304)..(318)
 187 <223> OTHER INFORMATION: Low-complexity sequence
 189 <220> FEATURE:
 190 <221> NAME/KEY: MISC_FEATURE
 191 <222> LOCATION: (416)..(436)
 192 <223> OTHER INFORMATION: Low-complexity sequence
 194 <400> SEQUENCE: 9
 196 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
 197 1 5 10 15
 200 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
 201 20 25 30
 204 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 205 35 40 45
 208 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Lys Lys

*(see item 8 on Error Summary Sheet)
for valid format*

*Do the same with
Sequences 43 and 44*

*yes, but which amino acid(s) do
the Xaa's represent?*

same error

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004

TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
 Output Set: N:\CRF4\12212004\J680963.raw

209	50	55	60
212	Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu		
213	65	70	75
216	Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly		80
217	85	90	95
220	Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met		
221	100	105	110
224	Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val		
225	115	120	125
228	Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys		
229	130	135	140
232	Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu		
233	145	150	155
236	Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys		160
237	165	170	175
240	Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala		
241	180	185	190
244	Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val		
245	195	200	205
248	Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu		
249	210	215	220
252	Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala		
253	225	230	235
256	Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln		240
257	245	250	255
260	Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu		
261	260	265	270
264	His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile		
265	275	280	285
W-->	268 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa		
269	290	295	300
272	Xaa Phe Val		
273	305	310	315
276	Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His		
277	325	330	335
280	Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile		
281	340	345	350
284	Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg		
285	355	360	365
288	Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile		
289	370	375	380
292	Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr		
293	385	390	395
296	Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa		400
297	405	410	415
300	Xaa		
301	420	425	430
304	Xaa Xaa Xaa Xaa Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg		
305	435	440	445

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/680,963
 DATE: 12/21/2004
 TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt
 Output Set: N:\CRF4\12212004\J680963.raw

308 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
 309 450 455
 312 <210> SEQ ID NO: 10
 313 <211> LENGTH: 458
 314 <212> TYPE: PRT
 315 <213> ORGANISM: *Saccharomyces cerevisiae*
 317 <400> SEQUENCE: 10
 319 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
 320 1 5 10 15
 323 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
 324 20 25 30
 327 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 328 35 40 45
 331 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
 332 50 55 60
 335 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
 336 65 70 75 80
 339 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
 340 85 90 95
 343 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
 344 100 105 110
 347 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
 348 115 120 125
 351 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
 352 130 135 140
 355 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
 356 145 150 155 160
 359 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
 360 165 170 175
 363 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
 364 180 185 190
 367 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
 368 195 200 205
 371 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
 372 210 215 220
 375 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
 376 225 230 235 240
 379 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
 380 245 250 255
 383 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
 384 260 265 270
 387 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
 388 275 280 285
 391 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
 392 290 295 300
 395 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
 396 305 310 315 320
 399 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
 400 325 330 335

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004
TIME: 11:33:41

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2
Seq#:2; Xaa Pos. 2
Seq#:5; N Pos. 9,12,18
Seq#:6; N Pos. 6,12
Seq#:9; Xaa Pos. 304,305,306,307,308,309,310,311,312,313,314,315,316,317
Seq#:9; Xaa Pos. 318,416,417,418,419,420,421,422,423,424,425,426,427,428
Seq#:9; Xaa Pos. 429,430,431,432,433,434,435,436
Seq#:11; Xaa Pos. 279,280,281,282,283,284,285,286,287,288,289,290,291,292
Seq#:11; Xaa Pos. 293
Seq#:25; Xaa Pos. 209,210,211,212,213,214,215,216,217,218,219,220,221,222
Seq#:25; Xaa Pos. 223,235,236,237,238,239,240,241,242,243,244,245,246
Seq#:27; Xaa Pos. 183,184,185,186,187,188,189,190,191,192,193,194,195,196
Seq#:27; Xaa Pos. 197,209,210,211,212,213,214,215,216,217,218,219,220
Seq#:29; Xaa Pos. 176,177,178,179,180,181,182,183,184,185,186,187,188,189
Seq#:29; Xaa Pos. 190,202,203,204,205,206,207,208,209,210,211,212,213
Seq#:31; Xaa Pos. 176,177,178,179,180,181,182,183,184,185,186,187,188,189
Seq#:31; Xaa Pos. 190,202,203,204,205,206,207,208,209,210,211,212,213
Seq#:75; N Pos. 17,20

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,41,42,47,48,49,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66
Seq#:67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,94
Seq#:95,96,97,98,99,100,101

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004

TIME: 11:33:41

Input Set : A:\GFI-108 Sequence listing.ST25.txt
Output Set: N:\CRF4\12212004\J680963.raw

L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:168 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:176 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:288
M:341 Repeated in SeqNo=9
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:272
M:341 Repeated in SeqNo=11
L:1467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:208
M:341 Repeated in SeqNo=25
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:176
M:341 Repeated in SeqNo=27
L:1909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:160
M:341 Repeated in SeqNo=29
L:2126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:160
M:341 Repeated in SeqNo=31
L:2547 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
L:2555 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:3343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0